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A Tale of Two Integrases: Genome Annotation of Novel Bacteriophage SavBucketDawg

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Bacteriophages (phages) are among the most ubiquitous biological entities on earth, with a population of more than 10e31 viruses. Because phages can lyse and kill bacteria, scientists are developing new methods to treat environmental problems by utilizing different types of phages, such as treating chlorine resistant filamentous *Gordonia* infestations. By characterizing novel phages we can improve phage applications in the medical and biotechnology fields. The novel *Gordonia terrae* phage Savbucketdawg was isolated and characterized from a soil sample taken in Saco, Maine (43°34'45.8"N 70°28'17.7"W). Savbucketdawg is a temperate and belongs to cluster DC1. The genome contains 57,801 bp with a GC content of 68% and 89 predicted protein-coding genes. Among those predicted genes, both a Tyrosine and a Serine integrase have been identified, along with numerous membrane proteins. Other notable findings in the Savbucketdawg genome include >99% shared nucleotide content with another cluster DC1 phage Jambalaya, an ASC-1 transcription coactivator, and a polynucleotide kinase. Electron microscopy was used to determine that Savbucketdawg (SBD) has Siphoviridae morphology with a long flexible tail (~303.33 ± 7.3 SE nm) and a capsid head ~60.85 ± 3.8 SE nm in diameter. The Savbucketdawg and Jambalaya genomes have unique features on their right arm that warrant further research.